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cont
- b) a naturally-occurring human polynucleotide sequence variant encoding an amino acid sequence having at least 90% sequence identity to the sequence of SEQ ID NO:1 and  
c) a polynucleotide sequence complementary to a) or b).
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Sub  
H1  
G3

20. A method of detecting a target polynucleotide in a sample, said target polynucleotide having the sequence of a polynucleotide of claim 19, comprising  
hybridizing the sample with a probe comprising at least 15 contiguous nucleotides comprising a sequence complementary to said target polynucleotide in the sample, and which probe specifically hybridizes to said target polynucleotide, under conditions whereby a hybridization complex is formed between said probe and said target polynucleotide, and  
detecting the presence or absence of said hybridization complex, and, optionally, if present, the amount thereof.

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21. A method of claim 20, wherein the probe comprises at least 30 contiguous nucleotides.

22. A method of claim 20, wherein the probe comprises at least 60 contiguous nucleotides.

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